WHAT IS CLAIMED IS:

1	1. A method of identifying an exon in a eukaryotic genomic fragment, the			
2	method comprising:			
3 expressing a population of subsequences of the genomic fragmen				
4	display library, wherein the population comprises protein-encoding subsequences and noncoding subsequences; screening the phage display library with a binding partner to identify an expressed subsequence that specifically binds to the binding partner; and mapping the expressed subsequence to the physical location in the genomic			
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9	fragment, thereby identifying the exon.			
1	2. The method of claim 1, wherein the binding partner is an antibody, an			
2	enzyme or a receptor.			
1	3. The method of claim 2, wherein the binding partner is an antibody.			
1	4. The method of claim 3, wherein the antibody is a single chain			
2	antibody.			
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2	5. The method of claim 1, wherein the binding partner is expressed by a			
2	phage display library.			
1	6. The method of claim 5, wherein the phage display library is an			
2	antibody phage display library generated using mRNA isolated from a stimulated B cell or a			
3	naïve B cell.			
1	7. The method of claim 6, wherein mRNA isolated from the stimulated B			
	cell is mRNA isolated from a stimulated splenic B cell that is isolated from an animal			
3	immunized with a composition comprising the protein epitope encoded by the genomic			
4	sequence or a nucleic acid encoding the protein epitope.			
	8. The method of claim 1, wherein the expressed subsequences are from			
2	about 100 base pairs to about 300 base pairs in length.			
1	9. The method of claim 1, wherein the genomic fragment is from a			
2	mammalian genome.			
	2 3 4 5 6 7 8 9 1 2 1 2 1 2 3 4 1 2 1			

1		10.	The method of claim 1, further wherein the exon is abnormally	
2	expressed in a cell of an individual with a disease or condition.			
1		11.	The method of claim 10, wherein the cell has a genomic translocation	
2	involving the	exon se	equence.	
1		12.	The method of claim 10, wherein the disease is cancer.	
1		13.	The method of claim 1, further comprising a step of enriching for	
2	phage expressing subsequences of the genomic fragment that are exons.			
1		14.	The method of claim 13, wherein the step of enriching comprises	
2	incubating the phage library with a binding partner specific for a peptide encoded by a			
3	subsequence that does not encode a peptide in vivo, and removing phage expressing the			
4	peptide from the library.			
1		15.	The method of claim 14, wherein the subsequence that does not encode	
2	a peptide in vi	vo is a	repetitive sequence.	
1		16.	The method of claim 15, wherein the repetitive sequence is an Alu	
2	sequence or a	Kpn se	•	
1		17		
1	1	17.	A phage display library comprising phage that express a population of	
2	subsequences of a eukaryotic genomic fragment, wherein the population comprises protein			
3	coding subseq	uences	and noncoding subsequences.	
1		18.	The phage display library of claim 11, wherein the eukaryotic genomic	
2	fragment is fro	om a m	ammalian genome.	
1		19.	The phage display library of claim 17, wherein the library is	
2	constructed us		BPM-1 vector.	
		8 P		
1		20.	The phage display library of claim 17, wherein the expressed	
2	subsequences	are from	m about 100 base pairs to about 300 base pairs in length.	

21. A phage expression vector comprising a polylinker region, an out-of-frame pIII gene, and at least one non-pallindromic rare cutting restriction enzyme site located

- in the polylinker site, wherein the non-pallindromic rare cutting restriction enzyme site is not located outside the polylinker region, and a selection tag encoding sequence.
- 1 22. The phage expression vector of claim 21, wherein the nonpallindromic rare cutting restriction enzyme site is an SfiI site.

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- 1 23. The phage expression vector of claim 21, wherein the selection tag is 2 an epitope tag selected from the group consisting of a polyhistidine tag or a myc tag.
- 1 24. The phage expression vector of claim 21, wherein the selection tag is an 2 antibiotic resistance polypeptide.
 - 25. A method of identifying an exon in a genomic fragment, the method comprising:

expressing a population of subsequences of the genomic fragment in a phage display library, wherein the population comprises protein-encoding subsequences and noncoding subsequences;

enriching for phage expressing subsequences of the genomic fragment that are exons;

screening the phage display library with a binding partner to identify an expressed subsequence that specifically binds to the binding partner; and

mapping the expressed subsequence to the physical location in the genomic fragment, thereby identifying the exon.

- 26. The method of claim 25, wherein the step of enriching comprises incubating the phage library with a binding partner specific for a peptide encoded by a subsequence that does not encode a peptide *in vivo*, and removing phage expressing the peptide from the library.
- 27. The method of claim 26, wherein the subsequence that does not encode a peptide *in vivo* is a repetitive sequence.
- 1 28. The method of claim 25, wherein the expressed subsequences are from 2 about 100 base pairs to about 300 base pairs in length.